

SEQUENCE LISTING

<110> Hellerqvist, Carl
Fu, Changlin

<120> GBS Toxin Receptor

<130> CARB-008/01US

<140>

<141>

<150> 60-693,843

<151> 1998-07-22

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 2602

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58) .. (1542)

<400> 1

```
tcgggccggc gctcccttct ctgccaggtg gcgagtacac ctgctcacgt aggcgtc      57

atg agg tct ccg gtt cga gac ctg gcc cgg aac gat ggc gag gag agc      105
Met Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser
   1             5             10             15

acg gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct      153
Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala
          20             25             30

cca gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt      201
Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe
          35             40             45

ggg ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta      249
Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu
          50             55             60

gtg gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc      297
```

Val	Asp	Met	Val	Asp	Ser	Asn	Thr	Thr	Leu	Glu	Asp	Asn	Arg	Thr	Ser		
65					70					75					80		
aag	gcg	tgt	cca	gag	cat	tct	gct	ccc	ata	aaa	gtt	cat	cat	aat	caa	345	
Lys	Ala	Cys	Pro	Glu	His	Ser	Ala	Pro	Ile	Lys	Val	His	His	Asn	Gln		
				85					90					95			
acg	ggt	aag	aag	tac	caa	tgg	gat	gca	gaa	act	caa	gga	tgg	att	ctc	393	
Thr	Gly	Lys	Lys	Tyr	Gln	Trp	Asp	Ala	Glu	Thr	Gln	Gly	Trp	Ile	Leu		
				100				105					110				
ggt	tcc	ttt	ttt	tat	ggc	tac	atc	atc	aca	cag	att	cct	gga	gga	tat	441	
Gly	Ser	Phe	Phe	Tyr	Gly	Tyr	Ile	Ile	Thr	Gln	Ile	Pro	Gly	Gly	Tyr		
		115					120					125					
gtt	gcc	agc	aaa	ata	ggg	ggg	aaa	atg	ctg	cta	gga	ttt	ggg	atc	ctt	489	
Val	Ala	Ser	Lys	Ile	Gly	Gly	Lys	Met	Leu	Leu	Gly	Phe	Gly	Ile	Leu		
	130						135					140					
ggc	act	gct	gtc	ctc	acc	ctg	ttc	act	ccc	att	gct	gca	gat	tta	gga	537	
Gly	Thr	Ala	Val	Leu	Thr	Leu	Phe	Thr	Pro	Ile	Ala	Ala	Asp	Leu	Gly		
145					150				155						160		
gtt	gga	cca	ctc	att	gta	ctc	aga	gca	cta	gaa	gga	cta	gga	gag	ggt	585	
Val	Gly	Pro	Leu	Ile	Val	Leu	Arg	Ala	Leu	Glu	Gly	Leu	Gly	Glu	Gly		
				165				170						175			
gtt	aca	ttt	cca	gcc	atg	cat	gcc	atg	tgg	tct	tct	tgg	gct	ccc	cct	633	
Val	Thr	Phe	Pro	Ala	Met	His	Ala	Met	Trp	Ser	Ser	Trp	Ala	Pro	Pro		
			180					185					190				
ctt	gaa	aga	agc	aaa	ctt	ctt	agc	att	tcg	tat	gca	gga	gca	cag	ctt	681	
Leu	Glu	Arg	Ser	Lys	Leu	Leu	Ser	Ile	Ser	Tyr	Ala	Gly	Ala	Gln	Leu		
		195					200					205					
ggg	aca	gta	att	tct	ctt	cct	ctt	tct	gga	ata	att	tgc	tac	tat	atg	729	
Gly	Thr	Val	Ile	Ser	Leu	Pro	Leu	Ser	Gly	Ile	Ile	Cys	Tyr	Tyr	Met		
	210					215					220						
aat	tgg	act	tat	gtc	ttc	tac	ttt	ttt	ggt	act	att	gga	ata	ttt	tgg	777	
Asn	Trp	Thr	Tyr	Val	Phe	Tyr	Phe	Phe	Gly	Thr	Ile	Gly	Ile	Phe	Trp		
225					230				235					240			
ttt	ctt	ttg	tgg	atc	tgg	tta	gtt	agt	gac	aca	cca	caa	aaa	cac	aag	825	
Phe	Leu	Leu	Trp	Ile	Trp	Leu	Val	Ser	Asp	Thr	Pro	Gln	Lys	His	Lys		
				245				250						255			
aga	att	tcc	cat	tat	gaa	aag	gaa	tac	att	ctt	tca	tca	tta	aga	aat	873	

Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn	
260	270
cag ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc	921
Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser	
275	285
ctg cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act	969
Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr	
290	300
ttt tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta	1017
Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu	
305	320
agg ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta	1065
Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu	
325	335
ggc tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta	1113
Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu	
340	350
agg gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc	1161
Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser	
355	365
ctt ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc	1209
Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe	
370	380
att ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca	1257
Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr	
385	400
aca ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat	1305
Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp	
405	415
att gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt	1353
Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe	
420	430
gcc act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc	1401
Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr	
435	445
cct gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct	1449

Pro	Asp	Asn	Thr	Val	Gly	Glu	Trp	Gln	Thr	Val	Phe	Tyr	Ile	Ala	Ala	
450						455					460					

gct att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt	1497
Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly	
465	470
	475
	480

gaa gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac	1542
Glu Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His	
485	490
	495

tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttattttatc atgtaacctc	1602
aaagtgcctt ctgtattgtg taagcattct atgtcttttt ttaattgtac ttgtattaga	1662
tttttaaggc ctataatcat gaaatatcac tagttgccag aataataaaa tgaactgtgt	1722
ttaattatga ataatatgta agctaggact tctacttttag gttcacatac ctgcctgcta	1782
gtcgggcaac atgaagtagg acagttctgt tgatttttta gggccatact aaagggaaatg	1842
agctgaaaca gacctcctga tacctttgct taattaaact agatgataat tctcaggtac	1902
tgataaacac ctgttgttgt tcactttcct cataaaaaatt gtcagctctc tctgacactt	1962
agacctcaaa ctttagcatc tctgtggagc tgccatccac tgtataattt cgcttgga	2022
ctggactgag gggagtgtgc ccaggcagct gccaagcact cctccctgg cttcagggtc	2082
agagtgccca gcgtttatca gaggcagcat ccaagcccag agccagtgtc gactcttcgg	2142
ctggtgcctt tcctctgagg ggctatcaat gtgtagataa agccctgagt aggcaagagc	2202
agtgagatcc actgctatgg tcttgataca tcctcaaact ttcccttccc agcacagagg	2262
aatattggct ggcattgcaac ctgcaaaaga aaaatgcgaa gcggccgggc acggtggctc	2322
atgcctgtaa tcccagcact ttggggggct gaggtgggag aatcatgaga tcaggagttc	2382
gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaattagct	2442
gggcgtgggtg acgggcgcct gtaatcccag atactcagga ggctgaggta ggagaatcac	2502
ttgaacctgg gaggtggaag ttgcagtga ccaagatcac gccactgcac tccagcctgg	2562
gcgatggagc gagactccaa ctcaaaaaaaaa aaaaaaaaaa	2602

<210> 2

<211> 495

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser
1 5 10 15

Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala
20 25 30

Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe
35 40 45

Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu
50 55 60

Val Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser
65 70 75 80

Lys Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln
85 90 95

Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
100 105 110

Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr
115 120 125

Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu
130 135 140

Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly
145 150 155 160

Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly
165 170 175

Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro
180 185 190

Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu
195 200 205

Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met
210 215 220

Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp
 225 230 235 240

Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys
 245 250 255

Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn
 260 265 270

Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser
 275 280 285

Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
 290 295 300

Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu
 305 310 315 320

Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu
 325 330 335

Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu
 340 345 350

Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser
 355 360 365

Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe
 370 375 380

Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
 385 390 395 400

Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
 405 410 415

Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
 420 425 430

Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr
 435 440 445

Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
 450 455 460

Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
 465 470 475 480

Glu Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
485 490 495

<210> 3
<211> 2844
<212> DNA
<213> Ovis sp.

<220>
<221> CDS
<222> (84)..(1568)

<400> 3
cccggggggcg gggggcttcg gcggtccgc tggagctctc ttttcgcgg agcaggtttg 60

cgccgtagct ccctgaaggc atc atg aag tcc ccg gtt tcg gac tta gcc ccg 113
Met Lys Ser Pro Val Ser Asp Leu Ala Pro
1 5 10

agc gac ggc gag gag ggc tcg gac cgc aca ccg ctc ctg cag cgc gcc 161
Ser Asp Gly Glu Glu Gly Ser Asp Arg Thr Pro Leu Leu Gln Arg Ala
15 20 25

ccg cgg gcg gaa ccc gct cca gta tgc tgc tct gct cgt tac aac cta 209
Pro Arg Ala Glu Pro Ala Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu
30 35 40

gca ttt ttg tcc ttt ttt ggt ttc ttc gtt ctc tat tca tta cgg gtg 257
Ala Phe Leu Ser Phe Phe Gly Phe Phe Val Leu Tyr Ser Leu Arg Val
45 50 55

aat ctg agc gtt gca cta gtg gac atg gtg gat tca aac aca act gcc 305
Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn Thr Thr Ala
60 65 70

aaa gat aat aga acg tcc tac gag tgt gca gag cat tct gct ccc ata 353
Lys Asp Asn Arg Thr Ser Tyr Glu Cys Ala Glu His Ser Ala Pro Ile
75 80 85 90

aaa gtt ctt cac aac caa acg ggt aaa aag tac cgg tgg gat gca gaa 401
Lys Val Leu His Asn Gln Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu
95 100 105

act caa gga tgg att ctc gga tct ttt ttc tat ggc tac atc atc aca 449
Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr
110 115 120

caa att cct gga gga tat gtt gcc agc aga agt ggg ggg aag ctg ttg	497
Gln Ile Pro Gly Gly Tyr Val Ala Ser Arg Ser Gly Gly Lys Leu Leu	
125 130 135	
cta gga ttc ggg atc ttt gct aca gct atc ttc acc ctg ttc act ccc	545
Leu Gly Phe Gly Ile Phe Ala Thr Ala Ile Phe Thr Leu Phe Thr Pro	
140 145 150	
ctc gct gca gat ttc gga gtc gga gcc ctt gtt gca ctc agg gca cta	593
Leu Ala Ala Asp Phe Gly Val Gly Ala Leu Val Ala Leu Arg Ala Leu	
155 160 165 170	
gaa ggg cta gga gag ggt gtc aca tat cca gcc atg cat gcc atg tgg	641
Glu Gly Leu Gly Glu Gly Val Thr Tyr Pro Ala Met His Ala Met Trp	
175 180 185	
tct tca tgg gct ccc cct ctt gaa aga agc aag ctt ctg agt att tca	689
Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser	
190 195 200	
tat gca gga gca caa ctt ggg aca gta gtt tct ctt cct ctt tct gga	737
Tyr Ala Gly Ala Gln Leu Gly Thr Val Val Ser Leu Pro Leu Ser Gly	
205 210 215	
gta att tgc tac tat atg aat tgg act tat gtc ttc tat ttc ttt ggc	785
Val Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly	
220 225 230	
att gtt gga atc atc tgg ttt att tta tgg atc tgc tta gtt agt gat	833
Ile Val Gly Ile Ile Trp Phe Ile Leu Trp Ile Cys Leu Val Ser Asp	
235 240 245 250	
aca cca gaa act cac aag aca atc act ccc tat gaa aag gag tat att	881
Thr Pro Glu Thr His Lys Thr Ile Thr Pro Tyr Glu Lys Glu Tyr Ile	
255 260 265	
ctt tca tca tta aaa aat cag ctc tct tca cag aag tca gtg ccg tgg	929
Leu Ser Ser Leu Lys Asn Gln Leu Ser Ser Gln Lys Ser Val Pro Trp	
270 275 280	
ata cct atg ctg aaa tca ctg cca ctt tgg gct att gtc gtt gca cat	977
Ile Pro Met Leu Lys Ser Leu Pro Leu Trp Ala Ile Val Val Ala His	
285 290 295	
ttt tct tac aac tgg act ttt tat act ttg ttg acc tta ttg cct act	1025
Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr	
300 305 310	

tac atg aag gaa gtc cta agg ttc aat att caa gag aat ggg ttt tta	1073
Tyr Met Lys Glu Val Leu Arg Phe Asn Ile Gln Glu Asn Gly Phe Leu	
315 320 325 330	
tct gca gtc cct tat tta ggt tgt tgg tta tgt atg atc ctg tcg ggt	1121
Ser Ala Val Pro Tyr Leu Gly Cys Trp Leu Cys Met Ile Leu Ser Gly	
335 340 345	
caa gct gct gac aat tta agg gca aga tgg aat ttt tca act ctg tgg	1169
Gln Ala Ala Asp Asn Leu Arg Ala Arg Trp Asn Phe Ser Thr Leu Trp	
350 355 360	
gtt cga aga gtt ttt agc ctt ata ggg atg att gga cct gcg ata ttc	1217
Val Arg Arg Val Phe Ser Leu Ile Gly Met Ile Gly Pro Ala Ile Phe	
365 370 375	
ctg gtt gcc gca gga ttt ata ggc tgt gat tat tcc ttg gct gtt gca	1265
Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala	
380 385 390	
ttc cta acc ata tca aca acc ctg gga ggc ttt tgc tct tct gga ttt	1313
Phe Leu Thr Ile Ser Thr Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe	
395 400 405 410	
agc atc aac cat ctg gac att gct cct tcg tat gct ggt att ctc ctg	1361
Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu	
415 420 425	
ggc atc aca aat acc ttt gcc act att cct gga atg att ggg ccc atc	1409
Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Ile Gly Pro Ile	
430 435 440	
att gcc aga agt ctt acc cct gag aac act att gga gaa tgg caa act	1457
Ile Ala Arg Ser Leu Thr Pro Glu Asn Thr Ile Gly Glu Trp Gln Thr	
445 450 455	
gtt ttc tgc atc gct gct gct atc aat gta ttt ggt gcc att ttc ttc	1505
Val Phe Cys Ile Ala Ala Ala Ile Asn Val Phe Gly Ala Ile Phe Phe	
460 465 470	
aca cta ttc gcc aaa ggt gaa gtg caa aac tgg gcc atc agt gat cac	1553
Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Ile Ser Asp His	
475 480 485 490	
caa gga cac aga aac tgaaggaacc aataaataat cctgtctcta ttaatgtatc	1608
Gln Gly His Arg Asn	
495	

ttgttttattc atgtaacctt aaagtgcctt tgatatttta atgtgtaagc aatctatata 1668
 caagataaaa ttgtactaga aaaattgtgt tagatttgta aggcttgtaa tcatgaaatg 1728
 tcatagttg ccatataagc aaaattagct atttttaatt attattaacc cgtttgctgg 1788
 aacttacaat tcaggggtcac atatctggct gcaagtcagg caaccacaa taggggagtt 1848
 ctatttattt ataagaccat acctaaagag atgagctgaa atagaccctt ctataccttt 1908
 gcttaattaa ggtggataat aattctcagg tcttggttaa catctgtttt tgtacacctt 1968
 cctcaaaaaa ttatttgta tcagcaatcc ctgacatgta ggtctcaaac tttagcctct 2028
 ccacggagct ggcagccact gtatcattca gcctggcaac ttcactgagg gaagcatgcc 2088
 caggcagctg ccacatgtcc cctctctggc ttcagggaca gtgcccagca cttaggcagc 2148
 atccaagacc aggggtcagcg ccaaggcttt ggacgggtatt cttccctgg ggctgttaat 2208
 gtgtggatga agccctgagc caacagggac agcgcgatcc acagtcatgg tttccatgca 2268
 ccctctccct tcccttccca gcacactgga gtattgcctg gcatgtaacc tgcaaaagaa 2328
 agtgtgatgc ctaattagcc acatataaca tcctccttga tgatcctacc ttcacatgga 2388
 tcagagtata aatcttcaag tctgtgttc taggagctac accagaataa ttaaaatata 2448
 aaaagaaaca aaacattttt tctgtctgac acctaagtgt ctggttgag ttcaagggtta 2508
 aagtgacttc tacttcacat aacctgcaac cgggtgtgta atcatcttta gtgttggttt 2568
 cttaaacttt atttttccag ttttctctgg accatcttcc agtggttttg agcatgcttt 2628
 gagggcattt atgtgattta gaacttgatt aatgtttcac tgtgtatgtt caacactacc 2688
 tgtaatatatt taactaaagc tatttaatgt aatatgatgt gtatacatc tgtaaattaa 2748
 tttttaaatc tgtaaatagc ttttaagttgc tatgggtgata tttcttttac aaatcaaaat 2808
 aaatcttttt ggaatgataa aaaaaaaaaa aaaaaa 2844

<210> 4

<211> 495

<212> PRT

<213> Ovis sp.

<400> 4

Met	Lys	Ser	Pro	Val	Ser	Asp	Leu	Ala	Pro	Ser	Asp	Gly	Glu	Glu	Gly	1	5	10	15
Ser	Asp	Arg	Thr	Pro	Leu	Leu	Gln	Arg	Ala	Pro	Arg	Ala	Glu	Pro	Ala	20	25	30	
Pro	Val	Cys	Cys	Ser	Ala	Arg	Tyr	Asn	Leu	Ala	Phe	Leu	Ser	Phe	Phe	35	40	45	
Gly	Phe	Phe	Val	Leu	Tyr	Ser	Leu	Arg	Val	Asn	Leu	Ser	Val	Ala	Leu	50	55	60	
Val	Asp	Met	Val	Asp	Ser	Asn	Thr	Thr	Ala	Lys	Asp	Asn	Arg	Thr	Ser	65	70	75	80
Tyr	Glu	Cys	Ala	Glu	His	Ser	Ala	Pro	Ile	Lys	Val	Leu	His	Asn	Gln	85	90	95	
Thr	Gly	Lys	Lys	Tyr	Arg	Trp	Asp	Ala	Glu	Thr	Gln	Gly	Trp	Ile	Leu	100	105	110	
Gly	Ser	Phe	Phe	Tyr	Gly	Tyr	Ile	Ile	Thr	Gln	Ile	Pro	Gly	Gly	Tyr	115	120	125	
Val	Ala	Ser	Arg	Ser	Gly	Gly	Lys	Leu	Leu	Leu	Gly	Phe	Gly	Ile	Phe	130	135	140	
Ala	Thr	Ala	Ile	Phe	Thr	Leu	Phe	Thr	Pro	Leu	Ala	Ala	Asp	Phe	Gly	145	150	155	160
Val	Gly	Ala	Leu	Val	Ala	Leu	Arg	Ala	Leu	Glu	Gly	Leu	Gly	Glu	Gly	165	170	175	
Val	Thr	Tyr	Pro	Ala	Met	His	Ala	Met	Trp	Ser	Ser	Trp	Ala	Pro	Pro	180	185	190	
Leu	Glu	Arg	Ser	Lys	Leu	Leu	Ser	Ile	Ser	Tyr	Ala	Gly	Ala	Gln	Leu	195	200	205	
Gly	Thr	Val	Val	Ser	Leu	Pro	Leu	Ser	Gly	Val	Ile	Cys	Tyr	Tyr	Met	210	215	220	
Asn	Trp	Thr	Tyr	Val	Phe	Tyr	Phe	Phe	Gly	Ile	Val	Gly	Ile	Ile	Trp	225	230	235	240
Phe	Ile	Leu	Trp	Ile	Cys	Leu	Val	Ser	Asp	Thr	Pro	Glu	Thr	His	Lys	245	250	255	

Thr Ile Thr Pro Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Lys Asn
 260 265 270
 Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Ile Pro Met Leu Lys Ser
 275 280 285
 Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
 290 295 300
 Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Val Leu
 305 310 315 320
 Arg Phe Asn Ile Gln Glu Asn Gly Phe Leu Ser Ala Val Pro Tyr Leu
 325 330 335
 Gly Cys Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu
 340 345 350
 Arg Ala Arg Trp Asn Phe Ser Thr Leu Trp Val Arg Arg Val Phe Ser
 355 360 365
 Leu Ile Gly Met Ile Gly Pro Ala Ile Phe Leu Val Ala Ala Gly Phe
 370 375 380
 Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
 385 390 395 400
 Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
 405 410 415
 Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
 420 425 430
 Ala Thr Ile Pro Gly Met Ile Gly Pro Ile Ile Ala Arg Ser Leu Thr
 435 440 445
 Pro Glu Asn Thr Ile Gly Glu Trp Gln Thr Val Phe Cys Ile Ala Ala
 450 455 460
 Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
 465 470 475 480
 Glu Val Gln Asn Trp Ala Ile Ser Asp His Gln Gly His Arg Asn
 485 490 495

<210> 5

<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 5
cgggatcccg ccngcnatgc ayrshrtstg g 31

<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 6
ggaattccdg gdgcratktc narrrrrtt 29

<210> 7
<211> 2930
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (263)..(1870)

<400> 7
gttcggtcga agccctcccc ttaattatgt gcaattcaag tccccactgc ccgcccgcga 60
gccccactc atcctcgctg cgggcagggt ggccctgca cttacaagg ggggtgcagga 120
gcgggagacg gtcgtccgaa caccggctcc ccggcatgcg tagaccggcg ggcggagcgg 180
gctcactttg cgccaatcct acgagaactc ccagaactcc gtttcctag tccaacccaa 240
gccagagttg cccacaccta ag atg gcg gcg ggg gcg atg aca ccg ccc cgc 292
Met Ala Ala Gly Ala Met Thr Pro Pro Arg
1 5 10

ccg gtc cag cca gct cgg ccc ggg ggc ttc ggg ctg tcg ggc cgg cgc 340
Pro Val Gln Pro Ala Arg Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg
15 20 25

tcc ctt ctc tgc cag gtg gcg agt aca cct gct cac gta ggc gtc atg	388
Ser Leu Leu Cys Gln Val Ala Ser Thr Pro Ala His Val Gly Val Met	
30 35 40	
agg tct ccg gtt cga gac ctg gcc cgg aac gat ggc gag gag agc acg	436
Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr	
45 50 55	
gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct cca	484
Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro	
60 65 70	
gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt ggt	532
Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly	
75 80 85 90	
ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta gtg	580
Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu Val	
95 100 105	
gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc aag	628
Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys	
110 115 120	
gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa acg	676
Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln Thr	
125 130 135	
ggg aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc ggt	724
Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly	
140 145 150	
tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat gtt	772
Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val	
155 160 165 170	
gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt ggc	820
Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu Gly	
175 180 185	
act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga gtt	868
Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly Val	
190 195 200	
gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt gtt	916
Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly Val	
205 210 215	

aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct ctt	964
Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro Leu	
220 225 230	
 gaa aga agc aaa ctt ctt agc att tgc tat gca gga gca cag ctt ggg	1012
Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly	
235 240 245 250	
 aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg aat	1060
Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn	
255 260 265	
 tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg ttt	1108
Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe	
270 275 280	
 ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag aga	1156
Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys Arg	
285 290 295	
 att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat cag	1204
Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln	
300 305 310	
 ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc ctg	1252
Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser Leu	
315 320 325 330	
 cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act ttt	1300
Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr Phe	
335 340 345	
 tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta agg	1348
Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg	
350 355 360	
 ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta ggc	1396
Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly	
365 370 375	
 tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta agg	1444
Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg	
380 385 390	
 gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc ctt	1492
Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser Leu	
395 400 405 410	

ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc att 1540
 Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile
 415 420 425

ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca aca 1588
 Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr
 430 435 440

ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat att 1636
 Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile
 445 450 455

gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc 1684
 Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala
 460 465 470

act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct 1732
 Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro
 475 480 485 490

gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct 1780
 Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala
 495 500 505

att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa 1828
 Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu
 510 515 520

gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac 1870
 Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
 525 530 535

tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttatttatac atgtaacctc 1930

aaagtgcctt ctgtattgtg taagcattct atgtcttttt ttaattgtac ttgtattaga 1990

ttttaaggc ctataatcat gaaatatcac tagttgccag aataataaaa tgaactgtgt 2050

ttaattatga ataatatgta agctaggact tctacttttag gttcacatac ctgcctgcta 2110

gtcgggcaac atgaagtagg acagttctgt tgatttttta gggccatact aaaggggaatg 2170

agctgaaaca gacctcctga tacctttgct taattaaact agatgataat tctcaggtac 2230

tgataaacac ctgttggtgt tcactttcct cataaaaatt gtcagctctc tctgacactt 2290

agacctcaaa ctttagcatc tctgtggagc tgccatccac tgtataattht cgctgggcaa 2350

ctggactgag gggagtgtgc ccaggcagct gccagcact cctccctgg cttcagggtc 2410
 agagtgccca gcgtttatca gaggcagcat ccaagcccag agccagtgtc gactcttcgg 2470
 ctggtgcctt tcctctgagg ggctatcaat gtgtagataa agccctgagt aggcaagagc 2530
 agtgagatcc actgctatgg tcttgatata tcctcaaact ttcccttccc agcacagagg 2590
 aatattggct ggcattgcaac ctgcaaaaaga aaaatgcaa gcggccgggc acggtgggtc 2650
 atgcctgtaa tcccagcact ttggggggct gaggtgggag aatcatgaga tcaggagtgc 2710
 gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaattagct 2770
 gggcggtggtg acgggcgcct gtaatcccag atactcagga ggctgaggta ggagaatcac 2830
 ttgaacctgg gaggtggaag ttgcagttaa ccaagatcac gccactgcac tccagcctgg 2890
 gcgatggagc gagactccaa ctcaaaaaaaaa aaaaaaaaaa 2930

<210> 8

<211> 536

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Gly Ala Met Thr Pro Pro Arg Pro Val Gln Pro Ala Arg
 1 5 10 15

Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg Ser Leu Leu Cys Gln Val
 20 25 30

Ala Ser Thr Pro Ala His Val Gly Val Met Arg Ser Pro Val Arg Asp
 35 40 45

Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr Asp Arg Thr Pro Leu Leu
 50 55 60

Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro Val Cys Cys Ser Ala Arg
 65 70 75 80

Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly Phe Phe Ile Val Tyr Ala
 85 90 95

Leu Arg Val Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn
 100 105 110

Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys Ala Cys Pro Glu His Ser	115	120	125
Ala Pro Ile Lys Val His His Asn Gln Thr Gly Lys Lys Tyr Gln Trp	130	135	140
Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr	145	150	155 160
Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val Ala Ser Lys Ile Gly Gly	165	170	175
Lys Met Leu Leu Gly Phe Gly Ile Leu Gly Thr Ala Val Leu Thr Leu	180	185	190
Phe Thr Pro Ile Ala Ala Asp Leu Gly Val Gly Pro Leu Ile Val Leu	195	200	205
Arg Ala Leu Glu Gly Leu Gly Glu Gly Val Thr Phe Pro Ala Met His	210	215	220
Ala Met Trp Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu	225	230	235 240
Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly Thr Val Ile Ser Leu Pro	245	250	255
Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr	260	265	270
Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe Leu Leu Trp Ile Trp Leu	275	280	285
Val Ser Asp Thr Pro Gln Lys His Lys Arg Ile Ser His Tyr Glu Lys	290	295	300
Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln Leu Ser Ser Gln Lys Ser	305	310	315 320
Val Pro Trp Val Pro Ile Leu Lys Ser Leu Pro Leu Trp Ala Ile Val	325	330	335
Val Ala His Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu	340	345	350
Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg Phe Asn Val Gln Glu Asn	355	360	365

Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly Ser Trp Leu Cys Met Ile
 370 375 380
 Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg Ala Lys Trp Asn Phe Ser
 385 390 395 400
 Thr Leu Cys Val Arg Arg Ile Phe Ser Leu Ile Gly Met Ile Gly Pro
 405 410 415
 Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu
 420 425 430
 Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly Gly Phe Cys Ser
 435 440 445
 Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly
 450 455 460
 Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Val
 465 470 475 480
 Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn Thr Val Gly Glu
 485 490 495
 Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn Val Phe Gly Ala
 500 505 510
 Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Leu
 515 520 525
 Asn Asp His His Gly His Arg His
 530 535

<210> 9

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human/sheep
consensus sequence

<220>

<221> CDS

<222> (1)..(1485)

<400> 9

atg arg tcy ccg gtt ysr gac ytr gcc csg arc gay ggc gag gag rgc	48
Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Glu Xaa	
1 5 10 15	
wcg gac cgc acr cck cty ctr cmg sgc gcc ccr cgg gcs gaa scc gct	96
Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala	
20 25 30	
cca gtr tgc tgc tct gct cgt tac aac yta gca wtt ttg kcc ttt ttt	144
Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe	
35 40 45	
ggg ttc ttc rtt sts tat kca tta cgg gtg aat ctg agy gtt gcr yta	192
Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa	
50 55 60	
gtg gay atg gtr gat tca aay aca act kym raa gat aat aga ack tcc	240
Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser	
65 70 75 80	
was gmg tgt sca gag cat tct gct ccc ata aaa gtt cwt cay aay caa	288
Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln	
85 90 95	
acg ggt aar aag tac crr tgg gat gca gaa act caa gga tgg att ctc	336
Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu	
100 105 110	
ggw tcy ttt tty tat ggc tac atc atc aca car att cct gga gga tat	384
Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr	
115 120 125	
gtt gcc agc ara akw ggg ggg aar mtg ytg cta gga tty ggg atc ytt	432
Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa	
130 135 140	
gsy acw gct rtc ytc acc ctg ttc act ccc mty gct gca gat ttm gga	480
Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly	
145 150 155 160	
gty gga scm cty rtt gya ctc agr gca cta gaa ggr cta gga gag ggt	528
Xaa Gly Xaa Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly	
165 170 175	
gty aca twt cca gcc atg cat gcc atg tgg tct tcw tgg gct ccc cct	576
Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro	
180 185 190	

ctt gaa aga agc aar ctt ctk agy att tcr tat gca gga gca car ctt	624
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu	
195 200 205	
ggg aca gta rtt tct ctt cct ctt tct gga rta att tgc tac tat atg	720
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met	
210 215 220	
aat tgg act tat gtc ttc tay tty ttt ggy ayt rtt gga atm wty tgg	720
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp	
225 230 235 240	
ttt mtt ttr tgg atc tgs tta gtt agt gay aca cca saa amw cac aag	768
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys	
245 250 255	
asa aty wcy cmy tat gaa aag gar tay att ctt tca tca tta ara aat	816
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn	
260 265 270	
cag cty tct tca cag aag tca gtg ccg tgg rta ccy atk ytr aaa tcm	864
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa	
275 280 285	
ctg cca ctt tgg gct aty gtm gtt gca cay ttt tct tac aac tgg act	912
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr	
290 295 300	
ttt tat act ttr ttg acm tta ttg cct act tay atg aag gar rtc cta	960
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu	
305 310 315 320	
agg ttc aat rtt caa gag aat ggg ttt tta tct kca kts cct tat tta	1008
Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu	
325 330 335	
ggy tst tgg tta tgt atg atc ctg tck ggt caa gct gct gac aat tta	1056
Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu	
340 345 350	
agg gca ara tgg aat ttt tca act ytr tgk gtt cgm aga rtt ttt agc	1104
Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser	
355 360 365	
ctt ata ggr atg att gga cct gcr rta ttc ctg gtw gcy gcw ggm tty	1152
Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa Xaa	
370 375 380	

atw ggc tgt gat tat tcy ttg gcy gtt gcw ttc cta acy ata tca aca 1200
 Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
 385 390 395 400

acm ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gay 1248
 Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
 405 410 415

att gct cct tcg tat gct ggt aty ctc ctg ggc atc aca aat acm ttt 1296
 Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
 420 425 430

gcc act att ccw gga atg rtt ggg ccc rtc att gcy ara agt ctk acc 1344
 Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
 435 440 445

cct gak aac act rtt gga gaa tgg caa acy gtk ttc try aty gct gct 1392
 Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
 450 455 460

gct aty aat gtw ttt ggt gcc att ttc tty aca cta ttc gcc aaa ggt 1440
 Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
 465 470 475 480

gaa gtr caa aac tgg gcy mtc art gat cac caw gga cac aga mac 1485
 Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa
 485 490 495

<210> 10

<211> 495

<212> PRT

<213> Artificial Sequence

<400> 10

Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Glu Xaa
 1 5 10 15

Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala
 20 25 30

Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe
 35 40 45

Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa
 50 55 60

Val	Xaa	Met	Xaa	Asp	Ser	Xaa	Thr	Thr	Xaa	Xaa	Asp	Asn	Arg	Xaa	Ser	65	70	75	80
Xaa	Xaa	Cys	Xaa	Glu	His	Ser	Ala	Pro	Ile	Lys	Val	Xaa	Xaa	Xaa	Gln	85	90	95	
Thr	Gly	Xaa	Lys	Tyr	Xaa	Trp	Asp	Ala	Glu	Thr	Gln	Gly	Trp	Ile	Leu	100	105	110	
Xaa	Xaa	Phe	Xaa	Tyr	Gly	Tyr	Ile	Ile	Thr	Xaa	Ile	Pro	Gly	Gly	Tyr	115	120	125	
Val	Ala	Ser	Xaa	Xaa	Gly	Gly	Xaa	Xaa	Xaa	Leu	Gly	Xaa	Gly	Ile	Xaa	130	135	140	
Xaa	Xaa	Ala	Xaa	Xaa	Thr	Leu	Phe	Thr	Pro	Xaa	Ala	Ala	Asp	Xaa	Gly	145	150	155	160
Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Ala	Leu	Glu	Xaa	Leu	Gly	Glu	Gly	165	170	175	
Xaa	Thr	Xaa	Pro	Ala	Met	His	Ala	Met	Trp	Ser	Xaa	Trp	Ala	Pro	Pro	180	185	190	
Leu	Glu	Arg	Ser	Xaa	Leu	Xaa	Xaa	Ile	Xaa	Tyr	Ala	Gly	Ala	Xaa	Leu	195	200	205	
Gly	Thr	Val	Xaa	Ser	Leu	Pro	Leu	Ser	Gly	Xaa	Ile	Cys	Tyr	Tyr	Met	210	215	220	
Asn	Trp	Thr	Tyr	Val	Phe	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Trp	225	230	235	240
Phe	Xaa	Xaa	Trp	Ile	Xaa	Leu	Val	Ser	Xaa	Thr	Pro	Xaa	Xaa	His	Lys	245	250	255	
Xaa	Xaa	Xaa	Xaa	Tyr	Glu	Lys	Xaa	Xaa	Ile	Leu	Ser	Ser	Leu	Xaa	Asn	260	265	270	
Gln	Xaa	Ser	Ser	Gln	Lys	Ser	Val	Pro	Trp	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	275	280	285	
Leu	Pro	Leu	Trp	Ala	Xaa	Xaa	Val	Ala	Xaa	Phe	Ser	Tyr	Asn	Trp	Thr	290	295	300	
Phe	Tyr	Thr	Xaa	Leu	Xaa	Leu	Leu	Pro	Thr	Xaa	Met	Lys	Xaa	Xaa	Leu	305	310	315	320

Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu
 325 330 335
 Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu
 340 345 350
 Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser
 355 360 365
 Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa Xaa
 370 375 380
 Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
 385 390 395 400
 Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
 405 410 415
 Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
 420 425 430
 Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
 435 440 445
 Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
 450 455 460
 Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
 465 470 475 480
 Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa
 485 490 495

<210> 11

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human/sheep
consensus sequence

<220>

<221> CDS

<222> (1)..(1485)

<400> 11

atg ang tcn ccg gtt nnn gac ntn gcc cng anc gan ggc gag gag ngc	48
Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Glu Xaa	
1 5 10 15	
ncg gac cgc acn ccn ctn ctn cng ngc gcc ccn cgg gcn gaa ncc gct	96
Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala	
20 25 30	
cca gtn tgc tgc tct gct cgt tac aac nta gca ntt ttg ncc ttt ttt	144
Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe	
35 40 45	
ggg ttc ttc ntt ntn tat nca tta cgn gtg aat ctg agn gtt gcn nta	192
Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa	
50 55 60	
gtg gan atg gtn gat tca aan aca act nnn naa gat aat aga acn tcc	240
Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser	
65 70 75 80	
nan gng tgt nca gag cat tct gct ccc ata aaa gtt cnt can aan caa	288
Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln	
85 90 95	
acg ggt aan aag tac cnn tgg gat gca gaa act caa gga tgg att ctc	336
Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu	
100 105 110	
ggn tcn ttt ttn tat ggc tac atc atc aca can att cct gga gga tat	384
Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr	
115 120 125	
gtt gcc agc ana ann ggg ggg aan ntg ntg cta gga ttn ggg atc ntt	432
Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa	
130 135 140	
gnn acn gct ntc ntc acc ctg ttc act ccc ntn gct gca gat ttn gga	480
Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly	
145 150 155 160	
gtn gga ncn ctn ntt gna ctc agn gca cta gaa ggn cta gga gag ggt	528
Xaa Gly Xaa Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly	
165 170 175	
gtn aca tnt cca gcc atg cat gcc atg tgg tct tcn tgg gct ccc cct	576
Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro	
180 185 190	

ctt gaa aga agc aan ctt ctn agn att tcn tat gca gga gca can ctt	624
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu	
195 200 205	
ggg aca gta ntt tct ctt cct ctt tct gga nta att tgc tac tat atg	672
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met	
210 215 220	
aat tgg act tat gtc ttc tan ttn ttt ggn ant ntt gga atn ntn tgg	720
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp	
225 230 235 240	
ttt ntt ttn tgg atc tgn tta gtt agt gan aca cca naa ann cac aag	768
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys	
245 250 255	
ana atn ncn cnn tat gaa aag gan tan att ctt tca tca tta ana aat	816
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn	
260 265 270	
cag ctn tct tca cag aag tca gtg ccg tgg nta ccn atn ntn aaa tcn	864
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa	
275 280 285	
ctg cca ctt tgg gct atn gtn gtt gca can ttt tct tac aac tgg act	912
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr	
290 295 300	
ttt tat act ttn ttg acn tta ttg cct act tan atg aag gan ntc cta	960
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu	
305 310 315 320	
agg ttc aat ntt caa gag aat ggg ttt tta tct nca ntn cct tat tta	1008
Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu	
325 330 335	
ggg tnt tgg tta tgt atg atc ctg tcn ggt caa gct gct gac aat tta	1056
Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu	
340 345 350	
agg gca ana tgg aat ttt tca act ntn tgn gtt cgn aga ntt ttt agc	1104
Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser	
355 360 365	
ctt ata ggn atg att gga cct gcg nta ttc ctg gtn gcg gcg ggn ttn	1152
Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa	
370 375 380	

atn ggc tgt gat tat tcn ttg gcn gtt gcn ttc cta acn ata tca aca 1200
 Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr
 385 390 395 400

acn ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gan 1248
 Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa
 405 410 415

att gct cct tcg tat gct ggt atn ctc ctg ggc atc aca aat acn ttt 1296
 Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe
 420 425 430

gcc act att ccn gga atg ntt ggg ccc ntc att gcn ana agt ctn acc 1344
 Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr
 435 440 445

cct gan aac act ntt gga gaa tgg caa acn gtn ttc tnn atn gct gct 1392
 Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala
 450 455 460

gct atn aat gtn ttt ggt gcc att ttc ttn aca cta ttc gcc aaa ggt 1440
 Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly
 465 470 475 480

gaa gtn caa aac tgg gcn ntc ant gat cac can gga cac aga nac 1485
 Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa
 485 490 495

<210> 12

<211> 495

<212> PRT

<213> Artificial Sequence

<400> 12

Met Xaa Xaa Pro Val Xaa Asp Xaa Ala Xaa Xaa Xaa Gly Glu Glu Xaa
 1 5 10 15

Xaa Asp Arg Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Arg Xaa Glu Xaa Ala
 20 25 30

Pro Xaa Cys Cys Ser Ala Arg Tyr Asn Xaa Ala Xaa Leu Xaa Phe Phe
 35 40 45

Gly Phe Phe Xaa Xaa Tyr Xaa Leu Xaa Val Asn Leu Xaa Val Xaa Xaa
 50 55 60

Val Xaa Met Xaa Asp Ser Xaa Thr Thr Xaa Xaa Asp Asn Arg Xaa Ser

65		70		75		80
Xaa Xaa Cys Xaa Glu His Ser Ala Pro Ile Lys Val Xaa Xaa Xaa Gln						
	85		90		95	
Thr Gly Xaa Lys Tyr Xaa Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu						
	100		105		110	
Xaa Xaa Phe Xaa Tyr Gly Tyr Ile Ile Thr Xaa Ile Pro Gly Gly Tyr						
	115		120		125	
Val Ala Ser Xaa Xaa Gly Gly Xaa Xaa Xaa Leu Gly Xaa Gly Ile Xaa						
	130		135		140	
Xaa Xaa Ala Xaa Xaa Thr Leu Phe Thr Pro Xaa Ala Ala Asp Xaa Gly						
	145		150		155	160
Xaa Gly Xaa Xaa Xaa Xaa Leu Xaa Ala Leu Glu Xaa Leu Gly Glu Gly						
	165		170		175	
Xaa Thr Xaa Pro Ala Met His Ala Met Trp Ser Xaa Trp Ala Pro Pro						
	180		185		190	
Leu Glu Arg Ser Xaa Leu Xaa Xaa Ile Xaa Tyr Ala Gly Ala Xaa Leu						
	195		200		205	
Gly Thr Val Xaa Ser Leu Pro Leu Ser Gly Xaa Ile Cys Tyr Tyr Met						
	210		215		220	
Asn Trp Thr Tyr Val Phe Xaa Xaa Phe Xaa Xaa Xaa Gly Xaa Xaa Trp						
	225		230		235	240
Phe Xaa Xaa Trp Ile Xaa Leu Val Ser Xaa Thr Pro Xaa Xaa His Lys						
	245		250		255	
Xaa Xaa Xaa Xaa Tyr Glu Lys Xaa Xaa Ile Leu Ser Ser Leu Xaa Asn						
	260		265		270	
Gln Xaa Ser Ser Gln Lys Ser Val Pro Trp Xaa Xaa Xaa Xaa Lys Xaa						
	275		280		285	
Leu Pro Leu Trp Ala Xaa Xaa Val Ala Xaa Phe Ser Tyr Asn Trp Thr						
	290		295		300	
Phe Tyr Thr Xaa Leu Xaa Leu Leu Pro Thr Xaa Met Lys Xaa Xaa Leu						
	305		310		315	320
Arg Phe Asn Xaa Gln Glu Asn Gly Phe Leu Ser Xaa Xaa Pro Tyr Leu						

325	330	335
Xaa Xaa Trp Leu Cys Met Ile Leu Xaa Gly Gln Ala Ala Asp Asn Leu		
340	345	350
Arg Ala Xaa Trp Asn Phe Ser Thr Xaa Xaa Val Xaa Arg Xaa Phe Ser		
355	360	365
Leu Ile Xaa Met Ile Gly Pro Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa Xaa		
370	375	380
Xaa Gly Cys Asp Tyr Xaa Leu Xaa Val Xaa Phe Leu Xaa Ile Ser Thr		
385	390	395
Xaa Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Xaa		
405	410	415
Ile Ala Pro Ser Tyr Ala Gly Xaa Leu Leu Gly Ile Thr Asn Xaa Phe		
420	425	430
Ala Thr Ile Xaa Gly Met Xaa Gly Pro Xaa Ile Xaa Xaa Ser Xaa Thr		
435	440	445
Pro Xaa Asn Thr Xaa Gly Glu Trp Gln Xaa Xaa Phe Xaa Xaa Ala Ala		
450	455	460
Ala Xaa Asn Xaa Phe Gly Ala Ile Phe Xaa Thr Leu Phe Ala Lys Gly		
465	470	475
Glu Xaa Gln Asn Trp Xaa Xaa Xaa Asp His Xaa Gly His Arg Xaa		
485	490	495